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RAW SEQUENCE LISTING

DATE: 03/27/2003

PATENT APPLICATION: US/09/762,568A

TIME: 13:23:06

Input Set : N:\Crf4\03272003\I762568.raw

Output Set: N:\CRF4\03272003\I762568A.raw

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1 <110> APPLICANT: Nippon Institute for Biological Science
2 <120> TITLE OF INVENTION: novel plasmid vector
3 <130> FILE REFERENCE: PCTF0001-0
4 <140> CURRENT APPLICATION NUMBER: US/09/762,568A
5 <141> CURRENT FILING DATE: 2001-02-06
6 <150> PRIOR APPLICATION NUMBER: JP, Japanese Patent
7 <151> PRIOR FILING DATE: 1999-06-04
8 <160> NUMBER OF SEQ ID NOS: 13
9 <170> SOFTWARE: FastSEQ for Windows Version 4.0
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 31
13 <212> TYPE: DNA
14 <213> ORGANISM: Artificial Sequence
15 <220> FEATURE:
16 <223> OTHER INFORMATION: Designed PCR primer including 3' region of U3 and
17     VspI restriction enzyme site to multiply RSV LTR.
18 <400> SEQUENCE: 1
19     ggcattaatg tagtcttatg caatactoct g                                     31
21 <210> SEQ ID NO: 2
22 <211> LENGTH: 40
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Designed PCR primer including 5' non coding region
27     of p19 gene, HincII, EcoRV and BglII restriction
28     enzyme site to multiply RSV LTR and down stream
29     region of LTR.
30 <400> SEQUENCE: 2
31     gttaacgata tcagatctgc ttgatccacc gggcgaccag                             40
33 <210> SEQ ID NO: 3
34 <211> LENGTH: 36
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Designed PCR primer including 5' region of RSV
39     integrase gene and BamHI restriction enzyme site
40     to multiply RSV integrase gene.
41 <400> SEQUENCE: 3
42     ttggatccat gcccttgaga gaggctaaag atcttc                               36
44 <210> SEQ ID NO: 4
45 <211> LENGTH: 33
46 <212> TYPE: DNA
47 <213> ORGANISM: Artificial Sequence

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48 <220> FEATURE:
49 <223> OTHER INFORMATION: Designed PCR primer including 3' region of RSV
50     integrase gene, polyA signal to multiply RSV
51     integrase gene.
52 <400> SEQUENCE: 4
53     tttatttttaa ctctcgttgg cagcaagggt gtc                                     33
55 <210> SEQ ID NO: 5
56 <211> LENGTH: 29
57 <212> TYPE: DNA
58 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Designed PCR primer including 5' region of U5 and
61     VspI restriction enzyme site to multiply RSV LTR.
62 <400> SEQUENCE: 5
63     ggcattaatg aagccttctg cttcattca                                         29
65 <210> SEQ ID NO: 6
66 <211> LENGTH: 51
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Designed PCR primer including 3' region of RSV
71     integrase gene, polyA signal, nuclear localization
72     signal of SV40 large T antigen to multiply RSV
73     integrase gene.
74 <400> SEQUENCE: 6
75     tttatttttaa accttcctct tcttcttagg actctcgttg gcagcaaggg t             51
77 <210> SEQ ID NO: 7
78 <211> LENGTH: 858
79 <212> TYPE: DNA
80 <213> ORGANISM: Rous sarcoma virus
81 <220> FEATURE:
82 <221> NAME/KEY: TATA_signal
83 <222> LOCATION: (84)...(90)
84 <220> FEATURE:
85 <221> NAME/KEY: polyA_signal
86 <222> LOCATION: (107)...(112)
87 <220> FEATURE:
88 <221> NAME/KEY: TATA_signal
89 <222> LOCATION: (431)...(437)
90 <220> FEATURE:
91 <221> NAME/KEY: polyA_signal
92 <222> LOCATION: (454)...(459)
93 <223> OTHER INFORMATION: A part of circular form of RSV DNA, tandem repeat
94     LTRs and adjacent non coding region.
95 <400> SEQUENCE: 7
96     acgatcgtgc cttattagga aggcaacaga cgggtctaac acggattgga cgaaccactg 60
97     aattccgcac tgcggagata ttgtatttaa gtgcctagct cgatacaata aacgccattt 120
98     taccattcac cacattggtg tgcacctggg ttgatggctg gaccgttgat tccctgacga 180
99     ctacgagcac atgcatgaag cagaaggctt cattaatgta gtcttatgca atactcctgt 240

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100 agtcttgcaa catgcttatg taacgatgag ttagcaacat gccttacaag gagagaaaag 300
101 gcaccgtgca cgacgattgg tggaaagtaag gtggtatgat cgtaggtacg atcgtgcctt 360
102 attaggaagg caacagacgg gtctaacacg gattggacga accactgaat tccgcattgc 420
103 ggagatattg tatttaagtg cctagctcga tacaataaac gccattttac cattcaccac 480
104 attggtgtgc acctgggttg atggctggac cgttgattcc ctgacgacta cgagcacatg 540
105 catgaagcag aaggcttcac ttggtgaccc cgacgtgacg gttaggggaat agtggtcggc 600
106 cacagacggc gtggcgatcc tgccctcatc cgtctcgctt attcggggag cggacgatga 660
107 ccctagtaga gggggctgcg gcttaggagg gcagaagctg agtggcgctc gagggagctc 720
108 tactgcaggg agcccagata ccctaccgag aactcagaga gtcgttgaa gacgggaaga 780
109 aagcccgcag actgagcggc ccaccccagg cgtgattccg gttgctctgc gtgaccctgg 840
110 tcgcccgggtg gatcaagc 858
112 <210> SEQ ID NO: 8
113 <211> LENGTH: 972
114 <212> TYPE: DNA
115 <213> ORGANISM: Rous sarcoma virus
116 <220> FEATURE:
117 <221> NAME/KEY: CDS
118 <222> LOCATION: (1)...(972)
119 <223> OTHER INFORMATION: precursor integrase or p36 protein
120 <220> FEATURE:
121 <221> NAME/KEY: CDS
122 <222> LOCATION: (1)...(858)
123 <223> OTHER INFORMATION: mature integrase or p32 protein
124 <400> SEQUENCE: 8
125 ccc ttg aga gag gct aaa gat ctt cat acc gct ctc cat att gga ccc 48
126 Pro Leu Arg Glu Ala Lys Asp Leu His Thr Ala Leu His Ile Gly Pro
127 1 5 10 15
128 cgc gcg cta tcc aaa gcg tgt aat ata tct atg cag cag gct agg gag 96
129 Arg Ala Leu Ser Lys Ala Cys Asn Ile Ser Met Gln Gln Ala Arg Glu
130 20 25 30
131 gtt gtt cag acc tgc ccg cat tgt aat tca gcc cct gcg ttg gag gcc 144
132 Val Val Gln Thr Cys Pro His Cys Asn Ser Ala Pro Ala Leu Glu Ala
133 35 40 45
134 gga gta aac cct agg ggt ttg gga ccc cta cag ata tgg cag aca gac 192
135 Gly Val Asn Pro Arg Gly Leu Gly Pro Leu Gln Ile Trp Gln Thr Asp
136 50 55 60
137 ttt acg ctt gag cct aga atg gcc ccc cgt tcc tgg ctc gct gtt act 240
138 Phe Thr Leu Glu Pro Arg Met Ala Pro Arg Ser Trp Leu Ala Val Thr
139 65 70 75 80
140 gtg gac acc gcc tca tca gcg ata gtc gta act cag cat ggc cgt gtc 288
141 Val Asp Thr Ala Ser Ser Ala Ile Val Val Thr Gln His Gly Arg Val
142 85 90 95
143 aca tcg gtt gct gta caa cat cat tgg gcc acg gct atc gcc gtt ttg 336
144 Thr Ser Val Ala Val Gln His His Trp Ala Thr Ala Ile Ala Val Leu
145 100 105 110
146 gga aga cca aag gcc ata aaa aca gat aac ggg tcc tgc ttc acg tct 384
147 Gly Arg Pro Lys Ala Ile Lys Thr Asp Asn Gly Ser Cys Phe Thr Ser
148 115 120 125
149 aaa tcc acg cga gag tgg ctc gcg aga tgg ggg ata gca cac acc acc 432

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150   Lys Ser Thr Arg Glu Trp Leu Ala Arg Trp Gly Ile Ala His Thr Thr
151       130                               135                       140
152   ggg att ccg ggt aat tcc cag ggt caa gct atg gta gag cgg gcc aac   480
153   Gly Ile Pro Gly Asn Ser Gln Gly Gln Ala Met Val Glu Arg Ala Asn
154       145                               150                       155                       160
155   cgg ctc ctg aaa gat agg atc cgt gtg ctt gcg gag ggg gac ggc ttt   528
156   Arg Leu Leu Lys Asp Arg Ile Arg Val Leu Ala Glu Gly Asp Gly Phe
157       165                               170                       175
158   atg aaa aga atc ccc acc agc aaa cag ggg gaa cta tta gcc aag gca   576
159   Met Lys Arg Ile Pro Thr Ser Lys Gln Gly Glu Leu Leu Ala Lys Ala
160       180                               185                       190
161   atg tat gcc ctc aat cac ttt gag cgt ggt gaa aac acg aaa aca ccg   624
162   Met Tyr Ala Leu Asn His Phe Glu Arg Gly Glu Asn Thr Lys Thr Pro
163       195                               200                       205
164   ata caa aaa cac tgg aga cct acc gtt ctt aca gaa gga ccc ccg gtt   672
165   Ile Gln Lys His Trp Arg Pro Thr Val Leu Thr Glu Gly Pro Pro Val
166       210                               215                       220
167   aaa ata cga ata gag aca ggg gag tgg gaa aaa gga tgg aac gtg ctg   720
168   Lys Ile Arg Ile Glu Thr Gly Glu Trp Glu Lys Gly Trp Asn Val Leu
169       225                               230                       235                       240
170   gtc tgg gga cga ggt tat gcc gct gtg aaa aac agg gac act gat aag   768
171   Val Trp Gly Arg Gly Tyr Ala Ala Val Lys Asn Arg Asp Thr Asp Lys
172       245                               250                       255
173   gtt att tgg gta ccc tct cga aaa gtt aaa ccg gac atc acc caa aag   816
174   Val Ile Trp Val Pro Ser Arg Lys Val Lys Pro Asp Ile Thr Gln Lys
175       260                               265                       270
176   gat gag gtg act aag aaa gat gag gcg agc cct ctt ttt gca ggc att   864
177   Asp Glu Val Thr Lys Lys Asp Glu Ala Ser Pro Leu Phe Ala Gly Ile
178       275                               280                       285
179   tct gac tgg ata ccc tgg gga gac aag caa gaa gga ctc caa gga gaa   912
180   Ser Asp Trp Ile Pro Trp Gly Asp Lys Gln Glu Gly Leu Gln Gly Glu
181       290                               295                       300
182   acc gct agc aac aag caa gaa aga ccc gga gaa gac acc ctt gct gcc   960
183   Thr Ala Ser Asn Lys Gln Glu Arg Pro Gly Glu Asp Thr Leu Ala Ala
184       305                               310                       315                       320
185   aac gag agt taa
186   Asn Glu Ser *   972
188 <210> SEQ ID NO: 9
189 <211> LENGTH: 21
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Designed PCR primer including 5' region of GFP
194   gene and a part ofNheI restriction enzyme site to
195   multiply GFP gene.
196 <400> SEQUENCE: 9
197   ctacgctac cggtcgccac c   21
199 <210> SEQ ID NO: 10
200 <211> LENGTH: 20

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201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Designed PCR primer including antisense sequence
205     of GFP ORF to multiply a part of GFP gene.
206 <400> SEQUENCE: 10
207     gttgccgtcc tccttgaagt                                20
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 21
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Designed PCR primer including U5 region LTR
215     sequence to
216     multiply a part of integrated plasmid vector.
217 <400> SEQUENCE: 11
218     ttggtgtgca cctgggttga t                                21
220 <210> SEQ ID NO: 12
221 <211> LENGTH: 36
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Designed PCR primer including 5' end of GFP ORF
226     sequence to multiply a part of GFP gene.
227 <400> SEQUENCE: 12
228     atggtgagca agggcgagga gctgttcacc ggggtg                36
230 <210> SEQ ID NO: 13
231 <211> LENGTH: 20
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Designed PCR primer including a part of GFP ORF
236     sequence to multiply a part of GFP gene.
237 <400> SEQUENCE: 13
238     gtcgagctgg acggcgacgt                                20

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/762,568A

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Input Set : N:\Crf4\03272003\I762568.raw

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